

IN THE CLAIMS

1. (Currently Amended) An isolated nucleic acid ~~virulent gene of *L. monocytogenes*,~~
wherein said nucleic acid comprises a sequence as set forth in SEQ ID NO:9 or is
complementary to SEQ ID NO:9.

2. (Currently Amended) The isolated ~~[[gene]]~~ nucleic acid of Claim 1, wherein said
nucleic acid ~~[[gene]]~~ encodes a protein having virulent biological activity.

3. (Currently Amended) The isolated ~~[[gene]]~~ nucleic acid of Claim 1, wherein a vector
comprises said ~~gene~~ comprises a nucleic acid molecule sequence ~~selected from the group~~
~~consisting of SEQ ID NOS.: 1-9.~~

4. (Currently Amended) The isolated ~~[[gene]]~~ nucleic acid of Claim 3, wherein ~~said gene~~
~~encodes a protein having virulent biological activity~~ a host cell comprises said vector.

5. (Canceled)

6. (Currently Amended) The isolated ~~[[gene]]~~ nucleic acid of Claim 1, wherein said
sequence ~~gene~~ comprises a nucleic acid molecule having 90 % sequence homology to a nucleic
acid molecule selected from the group consisting of SEQ ID NOS.: 1-9 comprises a contiguous
reading frame from about residue 887 to 1500 of SEQ ID NO:9.

7. (Currently Amended) The isolated ~~[[gene]]~~ nucleic acid of Claim 6[[1]], wherein said
~~gene~~ comprises a nucleic acid molecule having 80 % sequence homology to a nucleic acid
molecule selected from the group consisting of SEQ ID NOS.: 1-9 complement specifically
hybridizes to said contiguous reading frame in an *L. monocytogenes* strain selected from the
group consisting of *L. monocytogenes* ATCC 19111 serovar 1, *L. monocytogenes* ATCC 19112
serovar 2, *L. monocytogenes* ATCC 19113 serovar 3, *L. monocytogenes* ATCC 19115 serovar
4b, *L. monocytogenes* ATCC 19116 serovar 4c, *L. monocytogenes* ATCC 19116 serovar 4d, *L.*

monocytogenes ATCC 19118 serovar 4e, *L. monocytogenes* ATCC 15313 serovar 1, *L. monocytogenes* EDG (NCTC 7973) serovar 1/2a, *L. monocytogenes* HCC7 serovar 1, *L. monocytogenes* HCC8 serovar 1, *L. monocytogenes* 168, *L. monocytogenes* 180, *L. monocytogenes* 418, *L. monocytogenes* 742, *L. monocytogenes* 874, *L. monocytogenes* 1002, *L. monocytogenes* 1084, and *L. monocytogenes* 1400.

8. (Currently Amended) The isolated ~~[[gene]]~~ nucleic acid of Claim 7~~[[1]]~~, wherein said gene comprises a nucleic acid molecule that binds to a specific primer or probe, said primer or probe being selected from the group consisting of SEQ ID NOS.:10-27 contiguous reading frame encodes an amino acid sequence 203 residues in length.

9. (Currently Amended) The isolated ~~[[gene]]~~ nucleic acid of Claim 1, wherein said sequence hybridizes to residues 479-1500 of SEQ ID NO:9 ~~gene comprises a nucleic acid molecule that binds to a polynucleotide fragment having 95 % sequence homology to a primer or probe selected from the group consisting of SEQ ID NOS.: 10-27.~~

10. (Currently Amended) The isolated ~~[[gene]]~~ nucleic acid of Claim 9 ~~[[1]]~~, wherein said gene comprises a nucleic acid molecule that binds to a polynucleotide fragment having 90 % sequence homology to a primer or probe selected from the group consisting of SEQ ID NOS.: 10-27 hybridizing sequence is SEQ ID NO:27.

11. (Canceled)

12. (Currently Amended) The isolated ~~[[gene]]~~ nucleic acid of Claim 1, wherein said gene comprises a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-9 sequence hybridizes to the complement of residues 887-900 of SEQ ID NO:9.

13. (Currently Amended) A novel ~~The isolated nucleic acid~~ of Claim 12, wherein said hybridizing sequence is SEQ ID NO:26 primer or probe for the identification of virulent genes of

~~*L. monocytogenes*, said primer or probe being a polynucleotide fragment of at least 10 base pairs that bind to or are complementary with a portion of at least one polynucleotide selected from the group consisting of SEQ ID NOS.: 1-9.~~

14. (Currently Amended) An isolated nucleic acid complex comprising:

a) at least two [[novel]] primers, wherein one of said at least two primers comprises a sequence as set forth in SEQ ID NO:26 or SEQ ID NO:27; and
b) a nucleic acid comprising a sequence as set forth in SEQ ID NO:9, wherein said nucleic acid is isolated from an *L. monocytogenes* strain or probe for the identification of virulent genes of *L. monocytogenes*, said primer or probe being selected from the group consisting of SEQ ID NOS.: 10-27.

15. (Withdrawn) A method of identifying virulent *A. L. monocytogenes* isolate comprising:

providing at least one primer or probe specific for a corresponding at least one virulence-specific gene of *L. monocytogenes*;

conducting PCR assay or hybridization using said at least one primer or probe to identify the presence of said corresponding at least one virulence-specific gene in said *L. monocytogenes* isolate.

16. (Withdrawn) The method of Claim 15, wherein said virulence-specific gene is selected from the group consisting of genes identified by SEQ ID NOS.: 1-9.

17. (Withdrawn) The method of Claim 15, wherein said at least one primer is selected from the group consisting of SEQ ID NOS.: 10-27.

18. (Withdrawn) The method of Claim 15, wherein said at least one primer or probe is two or more primers or probes and said corresponding at least one virulence-specific gene is two

or more virulence-specific genes and said PCR assay or hybridization is multiplex polymerase chain reaction or hybridization.

19. (Withdrawn) The method of Claim 15, wherein said PCR assay or hybridization is multiplex polymerase chain reaction or hybridization using said primers or probes specific for said virulence-specific gene in combination with *Listeria* genus-specific primers or probes or *L. monocytogenes* species-specific gene sequence.

20. (Withdrawn) The method of Claim 15, wherein said *L. monocytogenes* species-specific gene sequence is selected from the from the group consisting of genes identified by SEQ ID NOS.: 28-33.

21. (Withdrawn) The method of Claim 15, wherein said PCR assay or hybridization is multiplex polymerase chain reaction or hybridization using said primers or probes specific for said virulence-specific gene in combination with *Listeria* genus-specific primers or probes and *L. monocytogenes* species-specific gene sequence.

22. (Withdrawn) The method of Claim 17, wherein said *L. monocytogenes* species-specific gene sequence is selected from the from the group consisting of genes identified by SEQ ID NOS.: 28-33.

23. (Withdrawn) The method of Claim 15, wherein said at least one virulence-specific gene is involved in inhibition of growth.

24. (Withdrawn) The method of Claim 15, wherein said at least one virulence-specific gene is involved in reduction of pathogenicity.

25. (Withdrawn) The method of Claim 15, wherein said at least one virulence-specific gene is involved in treatment of pathogenicity.

26. (Withdrawn) The method of Claim 15, wherein said at least one virulence-specific gene is involved in the prevention of virulent strains of *L. monocytogenes*.

27. (Withdrawn) The method of Claim 15, wherein said at least one virulence-specific gene is detected by amplification of said genes from mRNA and said PCR is reverse transcriptase-PCR (RT-PCR).

28. (Withdrawn) A method of identifying viable virulent strains of *L. monocytogenes* comprising:

providing at least one primer specific for a corresponding at least one virulence-specific gene of *L. monocytogenes*;

using said at least one primer to identify said at least one gene and amplifying sequence of said gene from from mRNA by reverse transcription-PCR (RT-PCR).

29. (Withdrawn) The method of Claim 28, wherein said virulence-specific gene is selected from the group consisting of SEQ ID NOS.: 1-9.

30. (Withdrawn) A method of treating a host subject in need of treatment for the pathogenic effects of a virulent strain of *L. monocytogenes* comprising:

administering an effective amount of at least one pharmaceutically active agent that is effective in altering or inactivating the function of at least one protein encoded by a virulence-specific gene.

31. (Withdrawn) The method of Claim 30, wherein said virulence-specific gene is selected from the group consisting of SEQ ID NOS.: 1-9.

32. (Withdrawn) The method of Claim 30, wherein said altering or inactivating kills said virulent strain of *L. monocytogenes*.

33. (Withdrawn) The method of Claim 30, wherein said altering or inactivating renders said virulent strain of *L. monocytogenes* susceptible to the immune system of said host subject.

34. (Withdrawn) A vaccine to protect a subject from the pathogenic effects of a virulent strain of *L. monocytogenes* comprising:

altering said at least one virulence-specific gene so as to render expression of the encoded protein of said at least one gene ineffective,

wherein said resulting *L. monocytogenes* is rendered avirulent and effective as a live attenuated bacteria suitable for use in a vaccine for said virulent strain of *L. monocytogenes*.

35. (Withdrawn) The method of Claim 34, wherein said virulence-specific gene is selected from the group consisting of SEQ ID NOS.: 1-9.

36. (Withdrawn) A method of vaccinating a subject to protect the subject from the pathogenic effects of a virulent strain of *L. monocytogenes* comprising:

administering a purified protein encoded by a virulence-specific gene or administering a live viral or bacterial vaccine expressing a protein encoded by a virulence-specific gene or administering a DNA vaccine comprising a virulence-specific gene.

37. (Withdrawn) The method of Claim 36, wherein said virulence-specific gene is selected from the group consisting of SEQ ID NOS.: 1-9.

38. (Withdrawn) A method of quickly determining if a sample taken from a food product contains a virulent strain of *L. monocytogenes*, the method comprising:

isolating *L. monocytogenes* from said food sample;

providing at least one primer specific for a corresponding at least one virulence-specific gene of *L. monocytogenes*;

conducting PCR assay using said at least one primer to identify the presence of said corresponding at least one virulence-specific gene in said *L. monocytogenes* isolate.

39. (Withdrawn) The method of Claim 38, wherein said virulence-specific gene is selected from the group consisting of SEQ ID NOS.: 1-9.

40. (New) The isolated nucleic acid complex of Claim 14, wherein said *L. monocytogenes* strain is selected from the group consisting of *L. monocytogenes* ATCC 19111 serovar 1, *L. monocytogenes* ATCC 19112 serovar 2, *L. monocytogenes* ATCC 19113 serovar 3, *L. monocytogenes* ATCC 19115 serovar 4b, *L. monocytogenes* ATCC 19116 serovar 4c, *L. monocytogenes* ATCC 19116 serovar 4d, *L. monocytogenes* ATCC 19118 serovar 4e, *L. monocytogenes* ATCC 15313 serovar 1, *L. monocytogenes* EDG (NCTC 7973) serovar 1/2a, *L. monocytogenes* HCC7 serovar 1, *L. monocytogenes* HCC8 serovar 1, *L. monocytogenes* 168, *L. monocytogenes* 180, *L. monocytogenes* 418, *L. monocytogenes* 742, *L. monocytogenes* 874, *L. monocytogenes* 1002, *L. monocytogenes* 1084, and *L. monocytogenes* 1400.